SEQUENCE LISTING

<110> Yano, Tetsuya; Nomoto, tsuyoshi; Imamura, Takeshi; Canon Kabushiki Kaisha

<120> DNA Fragment Carrying Toluene Monooxygenase Gene, Recombinant Plasmid, Transformed Microorganism, Method for Degrading Chlorinated Aliphatic Hydrocarbon Compounds and Aromatic Compounds, and Method for Environmental Remediation

<130> CFO13982US

<140> 09/430029
<141> 1999-10-29

<150> JP P1998-310801
<151> 1998-10-30

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<170> PatentIn Ver. 2.1

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aat cag cac ccc acc gat ctt tcc ccg ttc gat ccc ggc cgc aag tgc 284
Asn Gln His Pro Thr Asp Leu Ser Pro Phe Asp Pro Gly Arg Lys Cys
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gtc cgc gtg acc ggc acg aac gcg cgc ggc ttc gtc gaa ttc gag ctg 332
Val Arg Val Thr Gly Thr Asn Ala Arg Gly Phe Val Glu Phe Glu Leu
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tcg atc ggc ggc gcg ccg gaa ctg tgc gtc gag ctg acg ttg tct cct 380
Ser Ile Gly Gly Ala Pro Glu Leu Cys Val Glu Leu Thr Leu Ser Pro
35 40 45

gcc gcc ttc gat gcg ttc tgc cgc gaa cag cag gtc acg cgg ctc gac 428

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Ala Ala Phe Asp Ala Phe Cys Arg Glu Gln Gln Val Thr Arg Leu Asp
 50                  55                  60                  65

gtc gaa gcg aac cca tgaccttgag gagcaagaa gtg acc atc gag ctg aag  480
Val Glu Ala Asn Pro                     Met Thr Ile Glu Leu Lys
                 70                                          75

aca gtc gac atc aag ccg ctc cgg cac acc ttt gcg cat gtc gcg cag   528
Thr Val Asp Ile Lys Pro Leu Arg His Thr Phe Ala His Val Ala Gln
             80                  85                  90

aac atc ggc ggc gac aag acg gcg acg cgc tac cag gaa ggc atg atg   576
Asn Ile Gly Gly Asp Lys Thr Ala Thr Arg Tyr Gln Glu Gly Met Met
         95                  100                 105

ggc gcg cag ccc cag gag aac ttc cat tac cgg ccg acc tgg gac ccg   624
Gly Ala Gln Pro Gln Glu Asn Phe His Tyr Arg Pro Thr Trp Asp Pro
    110                 115                 120

gac tac gag atc ttc gat ccg tcg cgc tcg gcg atc cgg atg gcg aac   672
Asp Tyr Glu Ile Phe Asp Pro Ser Arg Ser Ala Ile Arg Met Ala Asn
125                 130                 135                 140

tgg tac gcg ttg aag gat ccg cgc cag ttc tac tac gcg tcg tgg gcg   720
Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe Tyr Tyr Ala Ser Trp Ala
                145                 150                 155

acc acg cgg gcg cgc cag cag gat gcg atg gag tcg aac ttc gag ttc   768
Thr Thr Arg Ala Arg Gln Gln Asp Ala Met Glu Ser Asn Phe Glu Phe
            160                 165                 170

gtc gaa tcg cgc cgg atg atc ggc ctg atg cgc gac gac gtg gcc gcg   816
Val Glu Ser Arg Arg Met Ile Gly Leu Met Arg Asp Asp Val Ala Ala
        175                 180                 185

cgg gcg ctc gac gtg ctg gtg ccg ctg cgc cac gcc gcg tgg ggc gcg   864
Arg Ala Leu Asp Val Leu Val Pro Leu Arg His Ala Ala Trp Gly Ala
    190                 195                 200

aac atg aac aac gcg cag atc tgc gcg ctc ggc tac ggc acg gtg ttc   912
Asn Met Asn Asn Ala Gln Ile Cys Ala Leu Gly Tyr Gly Thr Val Phe
205                 210                 215                 220

acc gcg ccc gcg atg ttc cat gcg atg gac aac ctc ggc gtc gcg caa   960
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Thr Ala Pro Ala Met Phe His Ala Met Asp Asn Leu Gly Val Ala Gln
                225                 230                 235

tac ctc acg cgt ctc gcg ctc gcg atg gcc gag ccc gac gtg ctg gag   1008
Tyr Leu Thr Arg Leu Ala Leu Ala Met Ala Glu Pro Asp Val Leu Glu
            240                 245                 250

gcg gcc aag gcg acc tgg acc cgc gac gcc gcc tgg cag ccg ctg cgc   1056
Ala Ala Lys Ala Thr Trp Thr Arg Asp Ala Ala Trp Gln Pro Leu Arg
        255                 260                 265

cgc tac gtc gag gac acg ctg gtc gtc gcc gat ccg gtc gag ctg ttc   1104
Arg Tyr Val Glu Asp Thr Leu Val Val Ala Asp Pro Val Glu Leu Phe
    270                 275                 280

atc gcg cag aac ctc gcg ctc gac ggc ctg ctg tat ccg ctc gtc tac   1152
Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu Leu Tyr Pro Leu Val Tyr
285                 290                 295                 300

gac cgc ttc gtc gac gaa cgg atc gcg ctc gaa ggc ggc tcg gca gtc   1200
Asp Arg Phe Val Asp Glu Arg Ile Ala Leu Glu Gly Gly Ser Ala Val
                305                 310                 315

gcg atg ctg acc gcg ttc atg ccc gaa tgg cac acc gag tcg aac cgc   1248
Ala Met Leu Thr Ala Phe Met Pro Glu Trp His Thr Glu Ser Asn Arg
            320                 325                 330

tgg atc gac gcg gtc gtg aag acg atg gcc gcc gaa tcc gac gac aac   1296
Trp Ile Asp Ala Val Val Lys Thr Met Ala Ala Glu Ser Asp Asp Asn
        335                 340                 345

cgc gcg ctg ctc gcc cgc tgg aca cgc gac tgg tcc gcg cgc gcc gag   1344
Arg Ala Leu Leu Ala Arg Trp Thr Arg Asp Trp Ser Ala Arg Ala Glu
    350                 355                 360

gcg gca ctg gca ccg gtg gcg gca cgc gcg ctg cag gat gcc ggg cgc   1392
Ala Ala Leu Ala Pro Val Ala Ala Arg Ala Leu Gln Asp Ala Gly Arg
365                 370                 375                 380

gcg gcg ctc gac gaa gtg cgc gag cag ttc cac gca cgc gcg gcc agg   1440
Ala Ala Leu Asp Glu Val Arg Glu Gln Phe His Ala Arg Ala Ala Arg
                385                 390                 395

ctc ggc atc gcg ctc tgacgacggg aatcctccct taacccaagg aatgccagc   1494
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a1 cont

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Leu Gly Ile Ala Leu
          400

atg tcc aac gta ttc atc gcc ttt cag gcc aat gag gac tcc aga ccg   1542
Met Ser Asn Val Phe Ile Ala Phe Gln Ala Asn Glu Asp Ser Arg Pro
            405                 410                 415

atc gtg gat gcg atc gtc gcc gac aac ccg cgc gcg gtg gtg gtc gag   1590
Ile Val Asp Ala Ile Val Ala Asp Asn Pro Arg Ala Val Val Val Glu
        420                 425                 430

tcg ccc ggc atg gtc aag atc gac gcg ccg gac cgg ctg acg atc cgc   1638
Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
    435                 440                 445

cgc gaa acg atc gag gaa ctg acc ggc acg cgc ttc gac ctg cag cag   1686
Arg Glu Thr Ile Glu Glu Leu Thr Gly Thr Arg Phe Asp Leu Gln Gln
450                 455                 460                 465

ctc cag gtc aac ctg atc acg ctg tca ggc cac atc gac gag gac gac   1734
Leu Gln Val Asn Leu Ile Thr Leu Ser Gly His Ile Asp Glu Asp Asp
                470                 475                 480

gac gag ttc acg ctg agc tgg tcg cac tgaacgccgc gccacgcgca         1781
Asp Glu Phe Thr Leu Ser Trp Ser His
            485                 490

ccgacaacac cggagacacg a atg gac acg cca acg ctc aag aaa aaa ctc   1832
                        Met Asp Thr Pro Thr Leu Lys Lys Lys Leu
                                    495                 500

ggc ctg aag gac cgc tac gcg gca atg acg cgc ggc ctc ggc tgg gag   1880
Gly Leu Lys Asp Arg Tyr Ala Ala Met Thr Arg Gly Leu Gly Trp Glu
                505                 510                 515

acg acc tac cag ccg atg gac aag gtc ttc ccg tac gac cgc tac gag   1928
Thr Thr Tyr Gln Pro Met Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu
            520                 525                 530

ggc atc aag atc cac gac tgg gac aag tgg gtc gac ccg ttc cgc ctg   1976
Gly Ile Lys Ile His Asp Trp Asp Lys Trp Val Asp Pro Phe Arg Leu
        535                 540                 545

acg atg gat gcg tac tgg aaa tac cag ggc gag aag gaa aag aag ctg   2024
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a' cont

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Thr Met Asp Ala Tyr Trp Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu
    550                 555                 560

tac gcg gtg atc gac gcg ttc acg cag aac aac gcg ttc ctc ggc gtg   2072
Tyr Ala Val Ile Asp Ala Phe Thr Gln Asn Asn Ala Phe Leu Gly Val
565                 570                 575                 580

agc gac gcc cgc tac atc aac gcg ctg aag ctg ttc ctc cag ggc gtg   2120
Ser Asp Ala Arg Tyr Ile Asn Ala Leu Lys Leu Phe Leu Gln Gly Val
                585                 590                 595

acg ccg ctc gaa tac ctc gcg cac cgc ggc ttc gcg cat gtc ggc cgg   2168
Thr Pro Leu Glu Tyr Leu Ala His Arg Gly Phe Ala His Val Gly Arg
            600                 605                 610

cac ttc acc ggc gag ggc gcg cgc atc gcg tgc cag atg cag tcg atc   2216
His Phe Thr Gly Glu Gly Ala Arg Ile Ala Cys Gln Met Gln Ser Ile
        615                 620                 625

gac gag ctg cgg cac tac cag acc gaa acg cat gcg atg tcg acg tac   2264
Asp Glu Leu Arg His Tyr Gln Thr Glu Thr His Ala Met Ser Thr Tyr
    630                 635                 640

aac aag ttc ttc aac ggg ttc cat cac tcg aac cag tgg ttc gac cgc   2312
Asn Lys Phe Phe Asn Gly Phe His His Ser Asn Gln Trp Phe Asp Arg
645                 650                 655                 660

gtg tgg tac ctg tcg gtg ccg aag tcg ttc ttc gag gac gcg tat tcg   2360
Val Trp Tyr Leu Ser Val Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser
                665                 670                 675

tcg ggg ccg ttc gag ttc ctg acc gcg gtc agc ttc tcg ttc gaa tac   2408
Ser Gly Pro Phe Glu Phe Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr
            680                 685                 690

gtg ctg acg aac ctg ctg ttc gtg ccg ttc atg tcg ggc gcc gcc tac   2456
Val Leu Thr Asn Leu Leu Phe Val Pro Phe Met Ser Gly Ala Ala Tyr
        695                 700                 705

aac ggt gac atg tcg acc gtc acg ttc ggc ttc tcc gcg cag tcg gac   2504
Asn Gly Asp Met Ser Thr Val Thr Phe Gly Phe Ser Ala Gln Ser Asp
    710                 715                 720

gaa tcg cgt cac atg acg ctc ggc atc gaa tgc atc aag ttc ctg ctc   2552
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a1 cont

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Glu Ser Arg His Met Thr Leu Gly Ile Glu Cys Ile Lys Phe Leu Leu
725                 730                 735                 740

gaa cag gac ccg gac aac gtg ccg atc gtg cag cgc tgg atc gac aag   2600
Glu Gln Asp Pro Asp Asn Val Pro Ile Val Gln Arg Trp Ile Asp Lys
                745                 750                 755

tgg ttc tgg cgc ggc tac cgg ctg ctg acg ctg gtc gcg atg atg atg   2648
Trp Phe Trp Arg Gly Tyr Arg Leu Leu Thr Leu Val Ala Met Met Met
            760                 765                 770

gac tac atg cag ccc aag cgc gtg atg agc tgg cgc gag tcg tgg gag   2696
Asp Tyr Met Gln Pro Lys Arg Val Met Ser Trp Arg Glu Ser Trp Glu
        775                 780                 785

atg tac gcc gag cag aac ggc ggc gcg ctg ttc aag gat ctc gcg cgc   2744
Met Tyr Ala Glu Gln Asn Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg
    790                 795                 800

tac ggc att cgc gag ccg aag ggc tgg cag gac gcc tgc gaa ggc aag   2792
Tyr Gly Ile Arg Glu Pro Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys
805                 810                 815                 820

gat cac atc agc cac cag gcg tgg tcg acg ttc tac ggc ttc aac gcg   2840
Asp His Ile Ser His Gln Ala Trp Ser Thr Phe Tyr Gly Phe Asn Ala
                825                 830                 835

gcc tcg gcg ttc cac acc tgg gtg ccg acc gaa gac gaa atg ggc tgg   2888
Ala Ser Ala Phe His Thr Trp Val Pro Thr Glu Asp Glu Met Gly Trp
            840                 845                 850

ctg tcg gcg aag tat ccc gac tcg ttc gac cgc tac tac cgc ccg cgc   2936
Leu Ser Ala Lys Tyr Pro Asp Ser Phe Asp Arg Tyr Tyr Arg Pro Arg
        855                 860                 865

ttc gat cac tgg ggc gag cag gcc agg gcc ggc aac cgc ttc tac atg   2984
Phe Asp His Trp Gly Glu Gln Ala Arg Ala Gly Asn Arg Phe Tyr Met
    870                 875                 880

aag acg ctg ccg atg ctg tgc cag acg tgc cag atc ccg atg ctg ttc   3032
Lys Thr Leu Pro Met Leu Cys Gln Thr Cys Gln Ile Pro Met Leu Phe
885                 890                 895                 900

acc gag ccg ggc aac ccg acg aag atc ggc gcg cgc gaa tcg aac tac   3080
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a' cont

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Thr Glu Pro Gly Asn Pro Thr Lys Ile Gly Ala Arg Glu Ser Asn Tyr
                905                 910                 915

ctc ggc aac aag ttc cac ttc tgc agc gac cac tgc aag gac atc ttc   3128
Leu Gly Asn Lys Phe His Phe Cys Ser Asp His Cys Lys Asp Ile Phe
            920                 925                 930

gat cac gag ccg cag aaa tac gtg cag gcg tgg ctg ccg gtg cac cag   3176
Asp His Glu Pro Gln Lys Tyr Val Gln Ala Trp Leu Pro Val His Gln
        935                 940                 945

atc cat cag ggc aac tgc ttc ccg ccc gat gcg gac ccg ggc gcg gag   3224
Ile His Gln Gly Asn Cys Phe Pro Pro Asp Ala Asp Pro Gly Ala Glu
    950                 955                 960

ggc ttc gat ccg ctc gcc gcg gtg ctc gac tac tac gcg gtg acg atg   3272
Gly Phe Asp Pro Leu Ala Ala Val Leu Asp Tyr Tyr Ala Val Thr Met
965                 970                 975                 980

ggc cgc gac aac ctc gat ttc gac ggc tcg gaa gac cag aag aac ttc   3320
Gly Arg Asp Asn Leu Asp Phe Asp Gly Ser Glu Asp Gln Lys Asn Phe
                985                 990                 995

gcg gcg tgg cgc ggc cag gcc acg cgc aac tgacccgcaa cgacaagcaa     3370
Ala Ala Trp Arg Gly Gln Ala Thr Arg Asn
           1000                1005

tcttgacgag ggcccgcgaa gcgccgatgc gcgaacgcgg gccgacagga gacaaac    3427

atg gcc gtc atc gcg ctc aaa ccc tac gac ttc ccg gtg aag gat gcc   3475
Met Ala Val Ile Ala Leu Lys Pro Tyr Asp Phe Pro Val Lys Asp Ala
         1010                1015                1020

gtc gag aag ttt ccg gcg ccg ctg ctc tac gtg tgc tgg gaa aac cat   3523
Val Glu Lys Phe Pro Ala Pro Leu Leu Tyr Val Cys Trp Glu Asn His
       1025                1030                1035

ctg atg ttc ccg gcg ccg ttc tgc ctg ccg ctg ccg ccc gac atg ccg   3571
Leu Met Phe Pro Ala Pro Phe Cys Leu Pro Leu Pro Pro Asp Met Pro
   1040                1045                1050

ttc ggc gcg ctg gcc ggc gac gtg ctg ccg ccc gtc tac ggc tat cac   3619
Phe Gly Ala Leu Ala Gly Asp Val Leu Pro Pro Val Tyr Gly Tyr His
1055                1060                1065                1070
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A' cont

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ccc gac ttc gcg aag atc gac tgg gat cgc gtc gag tgg ttc cgg tcg   3667
Pro Asp Phe Ala Lys Ile Asp Trp Asp Arg Val Glu Trp Phe Arg Ser
               1075                1080                1085

ggc gag ccg tgg gcg ccg gac ccg gcg aag agc ctg gcc ggc aac ggc   3715
Gly Glu Pro Trp Ala Pro Asp Pro Ala Lys Ser Leu Ala Gly Asn Gly
           1090                1095                1100

ctc ggg cac aag gac ctg atc agc ttc cgc acg ccc ggc ctc gac ggc   3763
Leu Gly His Lys Asp Leu Ile Ser Phe Arg Thr Pro Gly Leu Asp Gly
       1105                1110                1115

ctc ggc ggc gcg agc ttc tgaccgccac gcggacgagc gaaccatc atg agc    3815
Leu Gly Gly Ala Ser Phe                                 Met Ser
   1120                                                 1125

cac caa ctt acc atc gag ccg ctg ggc gtc acg atc gag gtc gag gaa   3863
His Gln Leu Thr Ile Glu Pro Leu Gly Val Thr Ile Glu Val Glu Glu
           1130                1135                1140

gga cag acg atg ctc gat gcc gcg ctg cgc cag ggc atc tac att ccg   3911
Gly Gln Thr Met Leu Asp Ala Ala Leu Arg Gln Gly Ile Tyr Ile Pro
       1145                1150                1155

cac gcg tgc tgt cac ggg ctg tgc ggc acc tgc aag gtc gcc gtg ctc   3959
His Ala Cys Cys His Gly Leu Cys Gly Thr Cys Lys Val Ala Val Leu
   1160                1165                1170

gac ggc gag acc gat ccc ggc gat gcg aac ccg ttc gcg ctg atg gat   4007
Asp Gly Glu Thr Asp Pro Gly Asp Ala Asn Pro Phe Ala Leu Met Asp
1175                1180                1185                1190

ttc gag cgc gag gaa ggc aag gcg ctc gcg tgc tgc gcg acg ctg cag   4055
Phe Glu Arg Glu Glu Gly Lys Ala Leu Ala Cys Cys Ala Thr Leu Gln
               1195                1200                1205

gcc gac acc gtg atc gag gcc gac gtc gac gag gag ccg gat gcg gaa   4103
Ala Asp Thr Val Ile Glu Ala Asp Val Asp Glu Glu Pro Asp Ala Glu
           1210                1215                1220

atc atc ccg gtc agg gac ttc gcg gcc gac gtc acg cgc atc gaa cag   4151
Ile Ile Pro Val Arg Asp Phe Ala Ala Asp Val Thr Arg Ile Glu Gln
       1225                1230                1235
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1 cont

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ctc acg ccg acc atc aag tcg atc cgc ctg aag ctg tcg cag ccg atc   4199
Leu Thr Pro Thr Ile Lys Ser Ile Arg Leu Lys Leu Ser Gln Pro Ile
   1240                1245                1250

cgc ttc cag gcg ggc cag tac gtg cag ctc gag att ccc ggc ctc ggg   4247
Arg Phe Gln Ala Gly Gln Tyr Val Gln Leu Glu Ile Pro Gly Leu Gly
1255                1260                1265                1270

cag agc cgc gcg ttc tcg atc gcg aac gcg ccg gcc gac gtc gcg gcc   4295
Gln Ser Arg Ala Phe Ser Ile Ala Asn Ala Pro Ala Asp Val Ala Ala
               1275                1280                1285

acc ggc gag atc gaa ctg aac gtg cgg cag gtg ccg ggc ggg ctc ggc   4343
Thr Gly Glu Ile Glu Leu Asn Val Arg Gln Val Pro Gly Gly Leu Gly
          1290                1295                1300

acg ggc tac ctg cac gag caa ctg gcg acg ggc gag cgc gtg cgc ctg   4391
Thr Gly Tyr Leu His Glu Gln Leu Ala Thr Gly Glu Arg Val Arg Leu
       1305                1310                1315

tcg ggc ccg tac ggc cgc ttc ttc gtg cgt cgc tcg gcc gcg cgg ccg   4439
Ser Gly Pro Tyr Gly Arg Phe Phe Val Arg Arg Ser Ala Ala Arg Pro
   1320                1325                1330

atg atc ttc atg gcc ggc ggg tcg ggg ctg tcg agc ccg cgc tcg atg   4487
Met Ile Phe Met Ala Gly Gly Ser Gly Leu Ser Ser Pro Arg Ser Met
1335                1340                1345                1350

atc gcg gac ctg ctc gca agc ggc gtc acc gcg ccg atc acg ctg gtc   4535
Ile Ala Asp Leu Leu Ala Ser Gly Val Thr Ala Pro Ile Thr Leu Val
               1355                1360                1365

tac ggt cag cgc agc gcg cag gag ctc tac tac cac gac gaa ttc cgc   4583
Tyr Gly Gln Arg Ser Ala Gln Glu Leu Tyr Tyr His Asp Glu Phe Arg
          1370                1375                1380

gcg ctg gcc gaa cgc cat ccg aac ttc acg tac gtg ccg gcg ctg tcc   4631
Ala Leu Ala Glu Arg His Pro Asn Phe Thr Tyr Val Pro Ala Leu Ser
       1385                1390                1395

gaa ggc gca ccg cac gcg ggc ggc gac gtc gcg caa ggg ttc gtg cac   4679
Glu Gly Ala Pro His Ala Gly Gly Asp Val Ala Gln Gly Phe Val His
   1400                1405                1410
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a1 cont.

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gac gtc gcg aag gca cat ttc ggc ggc gac ttc tcc ggg cac cag gcg   4727
Asp Val Ala Lys Ala His Phe Gly Gly Asp Phe Ser Gly His Gln Ala
1415                1420                1425                1430

tac ctg tgc ggg ccg ccc gcg atg atc gac gcg tgc atc acg acg ctg   4775
Tyr Leu Cys Gly Pro Pro Ala Met Ile Asp Ala Cys Ile Thr Thr Leu
                1435                1440                1445

atg cag ggg cgc ctg ttc gag cgc gac atc tat cac gag aag ttc atc   4823
Met Gln Gly Arg Leu Phe Glu Arg Asp Ile Tyr His Glu Lys Phe Ile
            1450                1455                1460

tcg gcg gcc gac gcg caa cag acg cgc agc ccg ctg ttc cgg cgg gtg   4871
Ser Ala Ala Asp Ala Gln Gln Thr Arg Ser Pro Leu Phe Arg Arg Val
        1465                1470                1475

tgac atg gac gcg ggc cgc gta tgc ggg acg gtc acg atc gcg cag acc  4920
     Met Asp Ala Gly Arg Val Cys Gly Thr Val Thr Ile Ala Gln Thr
        1480                1485                1490

gac gag cgc tat gcg tgc gtg tcc ggc gag tcg ctg ctg gcc ggc atg   4968
Asp Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met
    1495                1500                1505

gcg aaa ctc ggc cgg cgc ggc att ccg gtc ggc tgc ctg aac ggc ggg   5016
Ala Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly
1510                1515                1520                1525

tgc ggc gtg tgc aag gtg cgc gtg ctg cgc ggt gcg gtg cgc aag ctc   5064
Cys Gly Val Cys Lys Val Arg Val Leu Arg Gly Ala Val Arg Lys Leu
                1530                1535                1540

ggg ccg atc agc cgt gcc cat gtg agc gcg gaa gaa gag aac gac ggc   5112
Gly Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Glu Asn Asp Gly
            1545                1550                1555

tac gcg ctt gcg tgc cgc gtc gtg ccg gac ggc gac gtc gaa ctc gaa   5160
Tyr Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu
        1560                1565                1570

gtg gcc ggc cgg ctc agg aag ccg ttc ttc tgc ggc atg gca tgt gcc   5208
Val Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala
    1575                1580                1585
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a' cont

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ggc acg gcg gcg atc aac aag taaccaggag gagactcacc atgggtgtga      5259
Gly Thr Ala Ala Ile Asn Lys
1590                1595

tgcgtattgg tcatgtcagt ctgaaggtga tggacatgga agcggcgctg cgtcattacg 5319

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<400> 2

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Cys Val Arg Val Thr Gly Thr Asn Ala Arg Gly Phe Val Glu Phe Glu
             20                  25                  30
Leu Ser Ile Gly Gly Ala Pro Glu Leu Cys Val Glu Leu Thr Leu Ser
         35                  40                  45
Pro Ala Ala Phe Asp Ala Phe Cys Arg Glu Gln Gln Val Thr Arg Leu
     50                  55                  60
Asp Val Glu Ala Asn Pro
 65                  70
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  1               5                  10                  15
Phe Ala His Val Ala Gln Asn Ile Gly Gly Asp Lys Thr Ala Thr Arg
             20                  25                  30
Tyr Gln Glu Gly Met Met Gly Ala Gln Pro Gln Glu Asn Phe His Tyr
         35                  40                  45
Arg Pro Thr Trp Asp Pro Asp Tyr Glu Ile Phe Asp Pro Ser Arg Ser
     50                  55                  60
Ala Ile Arg Met Ala Asn Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe
 65                  70                  75                  80
Tyr Tyr Ala Ser Trp Ala Thr Thr Arg Ala Arg Gln Gln Asp Ala Met
                85                  90                  95
Glu Ser Asn Phe Glu Phe Val Glu Ser Arg Arg Met Ile Gly Leu Met
            100                 105                 110
Arg Asp Asp Val Ala Ala Arg Ala Leu Asp Val Leu Val Pro Leu Arg
        115                 120                 125
His Ala Ala Trp Gly Ala Asn Met Asn Asn Ala Gln Ile Cys Ala Leu
    130                 135                 140
Gly Tyr Gly Thr Val Phe Thr Ala Pro Ala Met Phe His Ala Met Asp
145                 150                 155                 160
Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Ala Met Ala
                165                 170                 175
Glu Pro Asp Val Leu Glu Ala Ala Lys Ala Thr Trp Thr Arg Asp Ala
            180                 185                 190
Ala Trp Gln Pro Leu Arg Arg Tyr Val Glu Asp Thr Leu Val Val Ala
        195                 200                 205
Asp Pro Val Glu Leu Phe Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu
    210                 215                 220
Leu Tyr Pro Leu Val Tyr Asp Arg Phe Val Asp Glu Arg Ile Ala Leu
225                 230                 235                 240
Glu Gly Gly Ser Ala Val Ala Met Leu Thr Ala Phe Met Pro Glu Trp
                245                 250                 255
His Thr Glu Ser Asn Arg Trp Ile Asp Ala Val Val Lys Thr Met Ala
            260                 265                 270
```

```
Ala Glu Ser Asp Asp Asn Arg Ala Leu Leu Ala Arg Trp Thr Arg Asp
        275                 280                 285
Trp Ser Ala Arg Ala Glu Ala Ala Leu Ala Pro Val Ala Ala Arg Ala
    290                 295                 300
Leu Gln Asp Ala Gly Arg Ala Ala Leu Asp Glu Val Arg Glu Gln Phe
305                 310                 315                 320
His Ala Arg Ala Ala Arg Leu Gly Ile Ala Leu
                325                 330
```

<210> 4
<211> 89
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomM polypeptide

<400> 4

```
Met Ser Asn Val Phe Ile Ala Phe Gln Ala Asn Glu Asp Ser Arg Pro
  1               5                  10                  15
Ile Val Asp Ala Ile Val Ala Asp Asn Pro Arg Ala Val Val Val Glu
             20                  25                  30
Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
         35                  40                  45
Arg Glu Thr Ile Glu Glu Leu Thr Gly Thr Arg Phe Asp Leu Gln Gln
     50                  55                  60
Leu Gln Val Asn Leu Ile Thr Leu Ser Gly His Ile Asp Glu Asp Asp
 65                  70                  75                  80
Asp Glu Phe Thr Leu Ser Trp Ser His
                85
```

<210> 5
<211> 516
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomN polypeptide

<400> 5

```
Met Asp Thr Pro Thr Leu Lys Lys Lys Leu Gly Leu Lys Asp Arg Tyr
  1               5                  10                  15
```

```
Ala Ala Met Thr Arg Gly Leu Gly Trp Glu Thr Thr Tyr Gln Pro Met
            20                  25                  30
Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu Gly Ile Lys Ile His Asp
        35                  40                  45
Trp Asp Lys Trp Val Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
    50                  55                  60
Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
65                  70                  75                  80
Phe Thr Gln Asn Asn Ala Phe Leu Gly Val Ser Asp Ala Arg Tyr Ile
                85                  90                  95
Asn Ala Leu Lys Leu Phe Leu Gln Gly Val Thr Pro Leu Glu Tyr Leu
            100                 105                 110
Ala His Arg Gly Phe Ala His Val Gly Arg His Phe Thr Gly Glu Gly
        115                 120                 125
Ala Arg Ile Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Tyr
    130                 135                 140
Gln Thr Glu Thr His Ala Met Ser Thr Tyr Asn Lys Phe Phe Asn Gly
145                 150                 155                 160
Phe His His Ser Asn Gln Trp Phe Asp Arg Val Trp Tyr Leu Ser Val
                165                 170                 175
Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser Ser Gly Pro Phe Glu Phe
            180                 185                 190
Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu
        195                 200                 205
Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
    210                 215                 220
Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
225                 230                 235                 240
Leu Gly Ile Glu Cys Ile Lys Phe Leu Leu Glu Gln Asp Pro Asp Asn
                245                 250                 255
Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
            260                 265                 270
Arg Leu Leu Thr Leu Val Ala Met Met Met Asp Tyr Met Gln Pro Lys
        275                 280                 285
Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Ala Glu Gln Asn
    290                 295                 300
Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Glu Pro
305                 310                 315                 320
Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
                325                 330                 335
Ala Trp Ser Thr Phe Tyr Gly Phe Asn Ala Ala Ser Ala Phe His Thr
            340                 345                 350
Trp Val Pro Thr Glu Asp Glu Met Gly Trp Leu Ser Ala Lys Tyr Pro
        355                 360                 365
```

a1 cont.

```
Asp Ser Phe Asp Arg Tyr Tyr Arg Pro Arg Phe Asp His Trp Gly Glu
    370                 375                 380
Gln Ala Arg Ala Gly Asn Arg Phe Tyr Met Lys Thr Leu Pro Met Leu
385                 390                 395                 400
Cys Gln Thr Cys Gln Ile Pro Met Leu Phe Thr Glu Pro Gly Asn Pro
                405                 410                 415
Thr Lys Ile Gly Ala Arg Glu Ser Asn Tyr Leu Gly Asn Lys Phe His
            420                 425                 430
Phe Cys Ser Asp His Cys Lys Asp Ile Phe Asp His Glu Pro Gln Lys
        435                 440                 445
Tyr Val Gln Ala Trp Leu Pro Val His Gln Ile His Gln Gly Asn Cys
    450                 455                 460
Phe Pro Pro Asp Ala Asp Pro Gly Ala Glu Gly Phe Asp Pro Leu Ala
465                 470                 475                 480
Ala Val Leu Asp Tyr Tyr Ala Val Thr Met Gly Arg Asp Asn Leu Asp
                485                 490                 495
Phe Asp Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Gln
            500                 505                 510
Ala Thr Arg Asn
        515
```

a1 cont

```
<210> 6
<211> 118
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomO polypeptide

<400> 6
Met Ala Val Ile Ala Leu Lys Pro Tyr Asp Phe Pro Val Lys Asp Ala
  1               5                  10                  15
Val Glu Lys Phe Pro Ala Pro Leu Leu Tyr Val Cys Trp Glu Asn His
             20                  25                  30
Leu Met Phe Pro Ala Pro Phe Cys Leu Pro Leu Pro Pro Asp Met Pro
         35                  40                  45
Phe Gly Ala Leu Ala Gly Asp Val Leu Pro Pro Val Tyr Gly Tyr His
     50                  55                  60
Pro Asp Phe Ala Lys Ile Asp Trp Asp Arg Val Glu Trp Phe Arg Ser
 65                  70                  75                  80
Gly Glu Pro Trp Ala Pro Asp Pro Ala Lys Ser Leu Ala Gly Asn Gly
                 85                  90                  95
Leu Gly His Lys Asp Leu Ile Ser Phe Arg Thr Pro Gly Leu Asp Gly
```

```
            100                 105                 110
Leu Gly Gly Ala Ser Phe
        115
```

<210> 7
<211> 354
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomP polypeptide

<400> 7

```
Met Ser His Gln Leu Thr Ile Glu Pro Leu Gly Val Thr Ile Glu Val
  1               5                  10                  15
Glu Glu Gly Gln Thr Met Leu Asp Ala Ala Leu Arg Gln Gly Ile Tyr
            20                  25                  30
Ile Pro His Ala Cys Cys His Gly Leu Cys Gly Thr Cys Lys Val Ala
        35                  40                  45
Val Leu Asp Gly Glu Thr Asp Pro Gly Asp Ala Asn Pro Phe Ala Leu
    50                  55                  60
Met Asp Phe Glu Arg Glu Glu Gly Lys Ala Leu Ala Cys Cys Ala Thr
65                  70                  75                  80
Leu Gln Ala Asp Thr Val Ile Glu Ala Asp Val Asp Glu Glu Pro Asp
                85                  90                  95
Ala Glu Ile Ile Pro Val Arg Asp Phe Ala Ala Asp Val Thr Arg Ile
            100                 105                 110
Glu Gln Leu Thr Pro Thr Ile Lys Ser Ile Arg Leu Lys Leu Ser Gln
        115                 120                 125
Pro Ile Arg Phe Gln Ala Gly Gln Tyr Val Gln Leu Glu Ile Pro Gly
    130                 135                 140
Leu Gly Gln Ser Arg Ala Phe Ser Ile Ala Asn Ala Pro Ala Asp Val
145                 150                 155                 160
Ala Ala Thr Gly Glu Ile Glu Leu Asn Val Arg Gln Val Pro Gly Gly
                165                 170                 175
Leu Gly Thr Gly Tyr Leu His Glu Gln Leu Ala Thr Gly Glu Arg Val
            180                 185                 190
Arg Leu Ser Gly Pro Tyr Gly Arg Phe Phe Val Arg Arg Ser Ala Ala
        195                 200                 205
Arg Pro Met Ile Phe Met Ala Gly Gly Ser Gly Leu Ser Ser Pro Arg
    210                 215                 220
Ser Met Ile Ala Asp Leu Leu Ala Ser Gly Val Thr Ala Pro Ile Thr
225                 230                 235                 240
```

```
Leu Val Tyr Gly Gln Arg Ser Ala Gln Glu Leu Tyr Tyr His Asp Glu
                245                 250                 255
Phe Arg Ala Leu Ala Glu Arg His Pro Asn Phe Thr Tyr Val Pro Ala
            260                 265                 270
Leu Ser Glu Gly Ala Pro His Ala Gly Gly Asp Val Ala Gln Gly Phe
        275                 280                 285
Val His Asp Val Ala Lys Ala His Phe Gly Gly Asp Phe Ser Gly His
    290                 295                 300
Gln Ala Tyr Leu Cys Gly Pro Pro Ala Met Ile Asp Ala Cys Ile Thr
305                 310                 315                 320
Thr Leu Met Gln Gly Arg Leu Phe Glu Arg Asp Ile Tyr His Glu Lys
                325                 330                 335
Phe Ile Ser Ala Ala Asp Ala Gln Gln Thr Arg Ser Pro Leu Phe Arg
            340                 345                 350
Arg Val
```

<210> 8
<211> 118
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomQ polypeptide

<400> 8

```
Met Asp Ala Gly Arg Val Cys Gly Thr Val Thr Ile Ala Gln Thr Asp
  1               5                  10                  15
Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met Ala
             20                  25                  30
Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly Cys
         35                  40                  45
Gly Val Cys Lys Val Arg Val Leu Arg Gly Ala Val Arg Lys Leu Gly
     50                  55                  60
Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Glu Asn Asp Gly Tyr
 65                  70                  75                  80
Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu Val
                 85                  90                  95
Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala Gly
            100                 105                 110
Thr Ala Ala Ile Asn Lys
        115
```

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 9
agtccgccat ggaggcgaca ccgatcatga atcagc 36

<210> 10
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 10
caccgaccat ggatcagcac cccaccgatc tttc 34

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 11
tgccgccttc catgggttct gccgcgaaca gcag 34

<210> 12
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 12
agcaagccat ggccatcgag ctgaagacag tcgacatca 39

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 13
ccgaccatca cctgctcggc cagatggaag tcgag 35